

**10/539634**  
**RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/539634  
Source: PCT  
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PCT

## RAW SEQUENCE LISTING

DATE: 06/27/2005

PATENT APPLICATION: US/10/539,634

TIME: 10:38:37

Input Set : A:\SEQ LIST WSU-10 (US).txt  
 Output Set: N:\CRF4\06272005\J539634.raw

3 <110> APPLICANT: CARLOCK, Leon  
 4 CYPHER, Maria  
 6 <120> TITLE OF INVENTION: Bioactive Peptides and Unique IRES Elements from  
 7 Myelin Proteolipid Protein PLP/DM20  
 9 <130> FILE REFERENCE: 2872-0010  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/539,634  
 C--> 12 <141> CURRENT FILING DATE: 2005-06-16  
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/39873  
 15 <151> PRIOR FILING DATE: 2003-12-16  
 17 <150> PRIOR APPLICATION NUMBER: US 60/433,573  
 18 <151> PRIOR FILING DATE: 2002-12-16  
 20 <160> NUMBER OF SEQ ID NOS: 40  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 850  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (1)..(831)  
 34 <400> SEQUENCE: 1  
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 36 Met Gly Leu Leu Glu Cys Cys Ala Arg Cys Leu Val Gly Ala Pro Phe  
 37 1 5 10 15  
 39 gct tcc ctg gtg gcc act gga ttg tgt ttc ttt ggg gtg gca ctg ttc 96  
 40 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe  
 41 20 25 30  
 43 tgt ggc tgt gga cat gaa gcc ctc act ggc aca gaa aag cta att gag 144  
 44 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu  
 45 35 40 45  
 47 acc tat ttc tcc aaa aac tac caa gac tat gag tat ctc atc aat gtg 192  
 48 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val  
 49 50 55 60  
 51 atc cat gcc ttc cag tat gtc atc tat gga act gcc tct ttc ttc 240  
 52 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe  
 53 65 70 75 80  
 55 ctt tat ggg gcc ctc ctg gct gag ggc ttc tac acc acc ggc gca 288  
 56 Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala  
 57 85 90 95  
 59 gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc 336  
 60 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly  
 61 100 105 110  
 63 ctg agc gca acg gta aca ggg ggc cag aag ggg agg ggt tcc aga ggc 384

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64 Leu Ser Ala Thr Val Thr Gly Gly Gln Lys Gly Arg Gly Ser Arg Gly  
 65 115 120 125  
 67 caa cat caa gct cat tct ttg gag cgg gtg tgt cat tgt ttg gga aaa 432  
 68 Gln His Gln Ala His Ser Leu Glu Arg Val Cys His Cys Leu Gly Lys  
 69 130 135 140  
 71 tgg cta gga cat ccc gac aag ttt gtg ggc atc acc tat gcc ctg acc 480  
 72 Trp Leu Gly His Pro Asp Lys Phe Val Gly Ile Thr Tyr Ala Leu Thr  
 73 145 150 155 160  
 75 gtt gtg tgg ctc ctg gtg ttt gcc tgc tct gct gtg ccc gtg tac att 528  
 76 Val Val Trp Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile  
 77 165 170 175  
 79 tac ttc aac acc tgg acc acc tgc gac tct att gcc ttc ccc agc aag 576  
 80 Tyr Phe Asn Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys  
 81 180 185 190  
 83 acc tct gcc agt ata ggc agt ctc tgt gct gac gcc aga atg tat ggt 624  
 84 Thr Ser Ala Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly  
 85 195 200 205  
 87 gtt ctc cca tgg aat gct ttc cct ggc aag gtt tgt ggc tcc aac ctt 672  
 88 Val Leu Pro Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu  
 89 210 215 220  
 91 ctg tcc atc tgc aaa aca gct gag ttc caa atg acc ttc cac ctg ttt 720  
 92 Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe  
 93 225 230 235 240  
 95 att gct gca ttt gtg ggg gct gca gct aca ctg gtt tcc ctg ctc acc 768  
 96 Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr  
 97 245 250 255  
 99 ttc atg att gct gcc act tac aac ttt gcc gtc ctt aaa ctc atg ggc 816  
 100 Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly  
 101 260 265 270  
 103 cga ggc acc aag ttc tgatacactg gttccctg 850  
 104 Arg Gly Thr Lys Phe  
 105 275  
 108 <210> SEQ ID NO: 2  
 109 <211> LENGTH: 277  
 110 <212> TYPE: PRT  
 111 <213> ORGANISM: Homo sapiens  
 113 <400> SEQUENCE: 2  
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 116 1 5 10 15  
 118 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe  
 119 20 25 30  
 121 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu  
 122 35 40 45  
 124 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val  
 125 50 55 60  
 127 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe  
 128 65 70 75 80  
 130 Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala  
 131 85 90 95

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133 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly  
 134 100 105 110  
 136 Leu Ser Ala Thr Val Thr Gly Gly Gln Lys Gly Arg Gly Ser Arg Gly  
 137 115 120 125  
 139 Gln His Gln Ala His Ser Leu Glu Arg Val Cys His Cys Leu Gly Lys  
 140 130 135 140  
 142 Trp Leu Gly His Pro Asp Lys Phe Val Gly Ile Thr Tyr Ala Leu Thr  
 143 145 150 155 160  
 145 Val Val Trp Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile  
 146 165 170 175  
 148 Tyr Phe Asn Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys  
 149 180 185 190  
 151 Thr Ser Ala Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly  
 152 195 200 205  
 154 Val Leu Pro Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu  
 155 210 215 220  
 157 Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe  
 158 225 230 235 240  
 160 Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr  
 161 245 250 255  
 163 Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly  
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 171 <211> LENGTH: 729  
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 176 <221> NAME/KEY: CDS  
 177 <222> LOCATION: (1)..(726)  
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 182 1 5 10 15  
 184 gct tcc ctg gtg gcc act gga ttg tgt ttc ttt ggg gtg gca ctg ttc 96  
 185 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe  
 186 20 25 30  
 188 tgt ggc tgt gga cat gaa gcc ctc act ggc aca gaa aag cta att gag 144  
 189 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu  
 190 35 40 45  
 192 acc tat ttc tcc aaa aac tac caa gac tat gag tat ctc atc aat gtg 192  
 193 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val  
 194 50 55 60  
 196 atc cat gcc ttc cag tat gtc atc tat gga act gcc tct ttc ttc ttc 240  
 197 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe  
 198 65 70 75 80  
 200 ctt tat ggg gcc ctc ctg ctg gct gag ggc ttc tac acc acc ggc gca 288  
 201 Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Gly Ala

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202	85	90	95	
204	gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc			336
205	Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly			
206	100	105	110	
208	ctg agc gca acg ttt gtg ggc atc acc tat gcc ctg acc gtt gtg tgg			384
209	Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp			
210	115	120	125	
212	ctc ctg gtg ttt gcc tgc tct gct gtg ccc gtg tac att tac ttc aac			432
213	Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile Tyr Phe Asn			
214	130	135	140	
216	acc tgg acc acc tgc gac tct att gcc ttc ccc agc aag acc tct gcc			480
217	Thr Trp Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala			
218	145	150	155	160
220	agt ata ggc agt ctc tgt gct gac gcc aga atg tat ggt gtt ctc cca			
221	Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly Val Leu Pro			
222	165	170	175	
224	tgg aat gct ttc cct ggc aag gtt tgt ggc tcc aac ctt ctg tcc atc			576
225	Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile			
226	180	185	190	
228	tgc aaa aca gct gag ttc caa atg acc ttc cac ctg ttt att gct gca			624
229	Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe Ile Ala Ala			
230	195	200	205	
232	ttt gtg ggg gct gca gct aca ctg gtt tcc ctg ctc acc ttc atg att			672
233	Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile			
234	210	215	220	
236	gct gcc act tac aac ttt gcc gtc ctt aaa ctc atg ggc cga ggc acc			
237	Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly Arg Gly Thr			
238	225	230	235	240
240	aag ttc tga			729
241	Lys Phe			
244	<210> SEQ ID NO: 4			
245	<211> LENGTH: 242			
246	<212> TYPE: PRT			
247	<213> ORGANISM: Homo sapiens			
249	<400> SEQUENCE: 4			
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254	Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe			
255	20	25	30	
257	Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu			
258	35	40	45	
260	Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val			
261	50	55	60	
263	Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe			
264	65	70	75	80
266	Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala			
267	85	90	95	
269	Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly			
270	100	105	110	

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272 Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp  
 273 115 120 125  
 275 Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile Tyr Phe Asn  
 276 130 135 140  
 278 Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala  
 279 145 150 155 160  
 281 Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly Val Leu Pro  
 282 165 170 175  
 284 Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile  
 285 180 185 190  
 287 Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe Ile Ala Ala  
 288 195 200 205  
 290 Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile  
 291 210 215 220  
 293 Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly Arg Gly Thr  
 294 225 230 235 240  
 296 Lys Phe  
 299 <210> SEQ ID NO: 5  
 300 <211> LENGTH: 216  
 301 <212> TYPE: DNA  
 302 <213> ORGANISM: Homo sapiens  
 304 <220> FEATURE:  
 305 <221> NAME/KEY: CDS  
 306 <222> LOCATION: (1)..(216)  
 308 <400> SEQUENCE: 5  
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 310 Met Tyr Gly Val Leu Pro Trp Asn Ala Phe Pro Gly Lys Val Cys Gly  
 311 1 5 10 15  
 313 tcc aac ctt ctg tcc atc tgc aaa aca gct gag ttc caa atg acc ttc 96  
 314 Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe  
 315 20 25 30  
 317 cac ctg ttt att gct gca ttt gtg ggg gct gca gct aca ctg gtt tcc 144  
 318 His Leu Phe Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser  
 319 35 40 45  
 321 ctg ctc acc ttc atg att gct gcc act tac aac ttt gcc gtc ctt aaa 192  
 322 Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys  
 323 50 55 60  
 325 ctc atg ggc cga ggc acc aag ttc 216  
 326 Leu Met Gly Arg Gly Thr Lys Phe  
 327 65 70  
 330 <210> SEQ ID NO: 6  
 331 <211> LENGTH: 72  
 332 <212> TYPE: PRT  
 333 <213> ORGANISM: Homo sapiens  
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 338 1 5 10 15  
 340 Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe  
 341 20 25 30

**VERIFICATION SUMMARY**

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Input Set : A:\SEQ LIST WSU-10 (US).txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date